

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/920,137G
Source: IFU/6
Date Processed by STIC: 1/19/06

ENTERED



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/920,137G

DATE: 01/19/2006
TIME: 12:23:51

Input Set : N:\SMITH\PTO.TS18.txt
Output Set: N:\CRF4\01192006\I920137G.raw

5 <110> APPLICANT: Giles-Komar, Jill; David Shealy; David Knight; Bernie
6 Scallon; George Heavner
8 <120> TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
10 <130> FILE REFERENCE: CEN0250 NP
12 <140> CURRENT APPLICATION NUMBER: US 09/920,137G
13 <141> CURRENT FILING DATE: 2001-08-01
15 <150> PRIOR APPLICATION NUMBER: 60/223,360
16 <151> PRIOR FILING DATE: 2000-08-07
18 <150> PRIOR APPLICATION NUMBER: 60/236,826
19 <151> PRIOR FILING DATE: 2000-09-29
21 <160> NUMBER OF SEQ ID NOS: 35
23 <170> SOFTWARE: PatentIn Ver 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 5
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: MISC_FEATURE
32 <222> LOCATION: (1)..(5)
33 <223> OTHER INFORMATION: Heavy Chain complementarity determining region 1 (CDR1).
36 <400> SEQUENCE: 1
38 Ser Tyr Ala Met His
39 1 5
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 17
44 <212> TYPE: PRT
45 <213> ORGANISM: Homo sapiens
47 <220> FEATURE:
48 <221> NAME/KEY: MISC_FEATURE
49 <222> LOCATION: (1)..(17)
50 <223> OTHER INFORMATION: Heavy Chain complementarity determining region 2 (CDR2).
52 <220> FEATURE:
53 <221> NAME/KEY: MISC_FEATURE /
54 <222> LOCATION: (1)..(1)
55 <223> OTHER INFORMATION: Xaa at position 1 is selected from Ile, Phe or Val.
57 <220> FEATURE:
58 <221> NAME/KEY: MISC_FEATURE
59 <222> LOCATION: (2)..(2) *✓*
60 <223> OTHER INFORMATION: Xaa at position 2 is selected from Ile or Met.
62 <220> FEATURE:
63 <221> NAME/KEY: MISC_FEATURE
64 <222> LOCATION: (3)..(3) *✓*
65 <223> OTHER INFORMATION: Xaa at position 3 is selected from Ser or Leu.

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67 <220> FEATURE:
68 <221> NAME/KEY: MISC_FEATURE
69 <222> LOCATION: (4)..(4)
70 <223> OTHER INFORMATION: Xaa at position 4 is selected from Tyr or Phe.
72 <220> FEATURE:
73 <221> NAME/KEY: MISC_FEATURE
74 <222> LOCATION: (10)..(10)
75 <223> OTHER INFORMATION: Xaa at position 10 is selected from Lys or Tyr.
77 <220> FEATURE:
78 <221> NAME/KEY: MISC_FEATURE
79 <222> LOCATION: (11)..(11)
80 <223> OTHER INFORMATION: Xaa at position 11 is selected from Ser or Tyr.
82 <220> FEATURE:
83 <221> NAME/KEY: MISC_FEATURE
84 <222> LOCATION: (17)..(17)
85 <223> OTHER INFORMATION: Xaa at position 17 is selected from Asp or Gly.
88 <400> SEQUENCE: 2
W--> 90 Xaa Xaa Xaa Xaa Asp Gly Ser Asn Lys Xaa Xaa Ala Asp Ser Val Lys Xaa
91 1 5 10 15
93 <210> SEQ ID NO: 3
94 <211> LENGTH: 17
95 <212> TYPE: PRT
96 <213> ORGANISM: Homo sapiens
98 <220> FEATURE:
99 <221> NAME/KEY: MISC_FEATURE
100 <222> LOCATION: (1)..(17)
101 <223> OTHER INFORMATION: Heavy Chain complementarity determining region 3 (CDR3).
103 <220> FEATURE:
104 <221> NAME/KEY: MISC_FEATURE
105 <222> LOCATION: (4)..(4)
106 <223> OTHER INFORMATION: Xaa at position 4 is selected from Ile or Val.
108 <220> FEATURE:
109 <221> NAME/KEY: MISC_FEATURE
110 <222> LOCATION: (5)..(5)
111 <223> OTHER INFORMATION: Xaa at position 5 is selected from Ser, Ala or Gly.
113 <220> FEATURE:
114 <221> NAME/KEY: MISC_FEATURE
115 <222> LOCATION: (9)..(9)
116 <223> OTHER INFORMATION: Xaa at position 9 is selected from Asn or Tyr.
118 <400> SEQUENCE: 3
W--> 120 Asp Arg Gly Xaa Xaa Ala Gly Gly Xaa Tyr Tyr Tyr Tyr Gly Met Asp Val
121 1 5 10 15
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 11
125 <212> TYPE: PRT
126 <213> ORGANISM: Homo sapiens
128 <220> FEATURE:
129 <221> NAME/KEY: MISC_FEATURE
130 <222> LOCATION: (1)..(11)

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131 <223> OTHER INFORMATION: Light Chain complementarity determining region 1 (CDR1).
 133 <220> FEATURE:
 134 <221> NAME/KEY: MISC_FEATURE
 135 <222> LOCATION: (7)..(7)
 136 <223> OTHER INFORMATION: Xaa at position 7 is selected from Ser or Tyr.
 138 <400> SEQUENCE: 4
 W--> 140 Arg Ala Ser Gln Ser Val Xaa Ser Tyr Leu Ala
 141 1 5 10
 143 <210> SEQ ID NO: 5
 144 <211> LENGTH: 7
 145 <212> TYPE: PRT
 146 <213> ORGANISM: Homo sapiens
 149 <220> FEATURE:
 150 <221> NAME/KEY: MISC_FEATURE
 151 <222> LOCATION: (1)..(7)
 152 <223> OTHER INFORMATION: Light Chain complementarity determining region 2 (CDR2).
 154 <400> SEQUENCE: 5
 156 Asp Ala Ser Asn Arg Ala Thr
 157 1 5
 159 <210> SEQ ID NO: 6
 160 <211> LENGTH: 10
 161 <212> TYPE: PRT
 162 <213> ORGANISM: Homo sapiens
 164 <220> FEATURE:
 165 <221> NAME/KEY: MISC_FEATURE
 166 <222> LOCATION: (1)..(10)
 167 <223> OTHER INFORMATION: Light Chain complementarity determining region 3 (CDR3).
 169 <400> SEQUENCE: 6
 171 Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr
 172 1 5 10
 174 <210> SEQ ID NO: 7
 175 <211> LENGTH: 126
 176 <212> TYPE: PRT
 177 <213> ORGANISM: Homo sapiens
 W--> 178 <400> SEQUENCE: 7
 180 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 181 1 5 10 15
 183 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
 184 20 25 30
 186 Ala Met His Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Val
 187 35 40 45
 189 Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala Asp Ser Val
 190 50 55 60
 192 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 193 65 70 75 80
 195 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 196 85 90 95
 198 Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr Tyr Gly
 199 100 105 110

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201 Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
202 115 120 125
206 <210> SEQ ID NO: 8
207 <211> LENGTH: 108
208 <212> TYPE: PRT
209 <213> ORGANISM: Homo sapiens
W--> 210 <400> SEQUENCE: 8
212 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
213 1 5 10 15
215 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Ser Tyr
216 20 25 30
218 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
219 35 40 45
221 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
222 50 55 60
224 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
225 65 70 75 80
227 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
228 85 90 95
230 Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
231 100 105
234 <210> SEQ ID NO: 9
235 <211> LENGTH: 157
236 <212> TYPE: PRT
237 <213> ORGANISM: Homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: MISC_FEATURE
241 <222> LOCATION: (1)..(157)
242 <223> OTHER INFORMATION: human TNF alpha monomer sequence
244 <400> SEQUENCE: 9
246 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
247 1 5 10 15
249 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
250 20 25 30
252 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
253 35 40 45
255 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
256 50 55 60
258 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
259 65 70 75 80
261 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
262 85 90 95
264 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
265 100 105 110
267 Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
268 115 120 125
270 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
271 130 135 140
273 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu

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Input Set : N:\SMITH\PTO.TS18.txt
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274	145	150	155
276	<210> SEQ ID NO: 10		
277	<211> LENGTH: 18		
278	<212> TYPE: DNA		
279	<213> ORGANISM: Homo sapiens		
281	<400> SEQUENCE: 10		
283	ttggtccagt cggactgg	18	
285	<210> SEQ ID NO: 11		
286	<211> LENGTH: 18		
287	<212> TYPE: DNA		
288	<213> ORGANISM: Homo sapiens		
290	<400> SEQUENCE: 11		
292	cacctgcact cggtgctt	18	
294	<210> SEQ ID NO: 12		
295	<211> LENGTH: 30		
296	<212> TYPE: DNA		
297	<213> ORGANISM: Homo sapiens		
299	<400> SEQUENCE: 12		
301	cactgtttg agtgtgtacg ggcttaagtt		30
303	<210> SEQ ID NO: 13		
304	<211> LENGTH: 18		
305	<212> TYPE: DNA		
306	<213> ORGANISM: Homo sapiens		
308	<400> SEQUENCE: 13		
310	gccgcacgtg tggaaggg	18	
312	<210> SEQ ID NO: 14		
313	<211> LENGTH: 25		
314	<212> TYPE: DNA		
315	<213> ORGANISM: Homo sapiens		
317	<400> SEQUENCE: 14		
319	agtcaaggc ggactggctt aagtt		25
321	<210> SEQ ID NO: 15		
322	<211> LENGTH: 28		
323	<212> TYPE: DNA		
324	<213> ORGANISM: Homo sapiens		
326	<400> SEQUENCE: 15		
328	gttgtccct ctcacaatct tcgaattt		28
330	<210> SEQ ID NO: 16		
331	<211> LENGTH: 18		
332	<212> TYPE: DNA		
333	<213> ORGANISM: Homo sapiens		
335	<400> SEQUENCE: 16		
337	ggcggtagac tactcgac	18	
340	<210> SEQ ID NO: 17		
341	<211> LENGTH: 7		
342	<212> TYPE: PRT		
343	<213> ORGANISM: Homo sapiens		
345	<400> SEQUENCE: 17		
347	Met Asp Trp Thr Trp Ser Ile		

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1,2,3,4,10,11,17
Seq#:3; Xaa Pos. 4,5,9
Seq#:4; Xaa Pos. 7

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:32; Line(s) 490
Seq#:33; Line(s) 508
Seq#:34; Line(s) 528
Seq#:35; Line(s) 550

VERIFICATION SUMMARY

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L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:178 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:283 W: Missing Blank Line separator, <400> field identifier